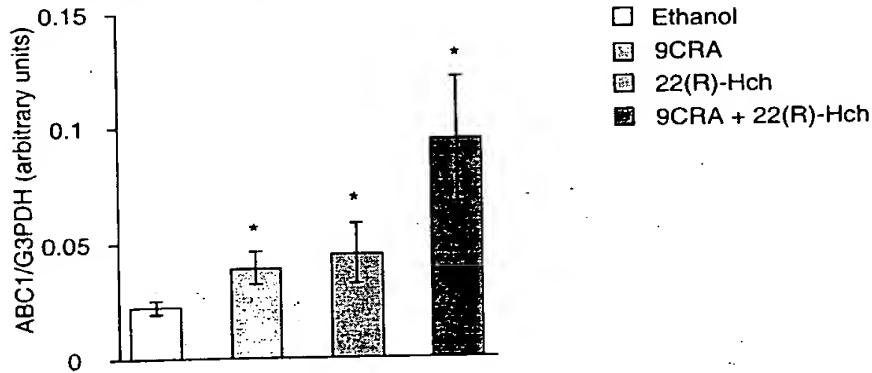
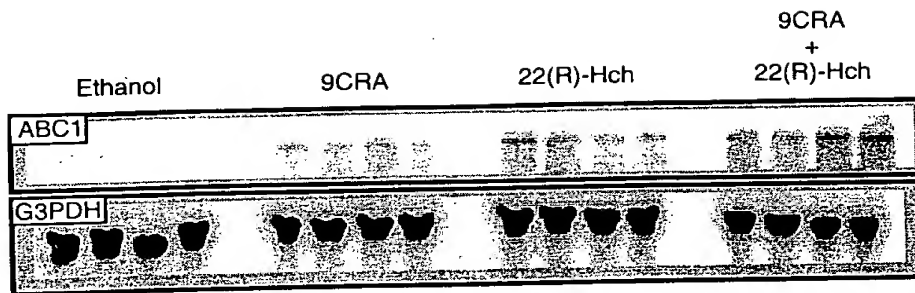


APPROVED	O.G. FIG.	
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FIG. 1



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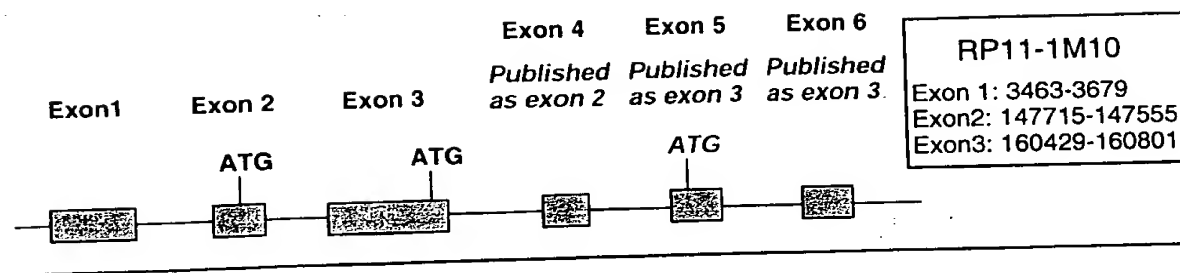
[illegible]

FIG. 2B

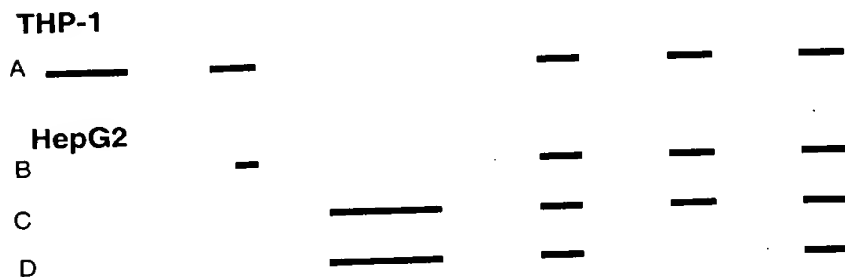


FIG. 2C

1 22 61  
A, B MACWPQLRVLLWKNLTFRRRQTCQLLLEVAWPLFIFILISVRLSYPPYEQHECHFNP  
C, D MCQLLLEVAWPLFIFILISVRLSYPPYEQHECHFNP

tBlastn result: Alignment between hABC1 and hABCR.  
Identical = 32/56 (57%), conservative = 12/56 (21%)

hABC1 6QLRVLLWKNLTFRRRQTCQLLLEVAWPLFIFILISVRLSYPPYEQHECHFPNKAM 61  
|..||| |.| |. || .|. |. |. |. |||||  
hABCR 6QIQLLLWNWTLRKQRKIRFVVVLVWPLSLFLVIWLNRNANPLYSHHECHFPNKAM 61

tBlastn result: Alignment between hABC1 and hABC3.  
Identical = 20/44 (45%), conservative = 7/44 (16%)

Identical = 20/44 (45%), conservative = 7/44 (16%)

hABC1	1MACWPQLRVLLWKNLTFRRRQTCQLLLEVAWPLFIFLILISVRL	44
	■      ■■ ■ ■  ■        ■	
hABC3	1MAVLRQLALLLWKNYTLQKRKVLTVLELFLPLLFSGILIWLRL	44

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FIG. 3

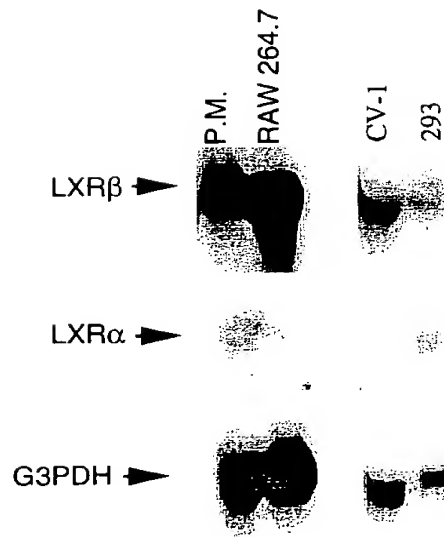
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 ggagattcagcctagagctctctctcccaatccctccctcgggtgaggaaactaacaaggaaaaaaa  
 attgcggaaagcaggatttagaggaagcaaattccactggtgcccttggctgccgggaacgtggactagag  
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 cgatagtaacctctgcgtcgggtgcagccgaatcTATAAaaggaaactagtccggcaaaaaccccgtaa  
 ttgcgagcgagagtgagtggggccgggacccgcagagccgagccgacccttctctcccggtg  
 cggcagggcagggcggggagctccgcgcaccaacagagc

CREBP1CJUN  
 -928bp  
 CEBPB  
 HNF3B  
 IRF1  
 NF-KB  
 Sac1  
 Stat1  
 MYC MAX  
 AP1  
 SP1  
 +101

003240.2509560

APPROVED	O.G. FIG.	
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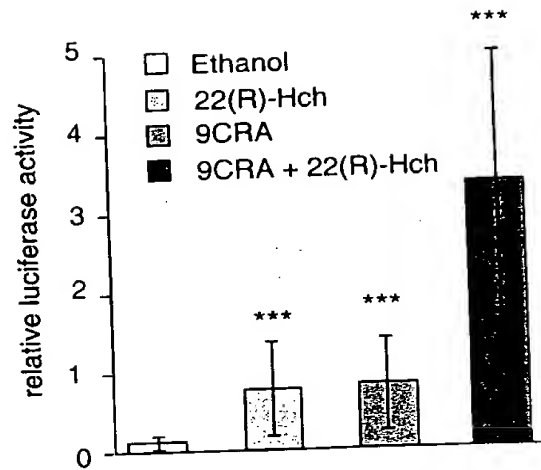
FIG. 4



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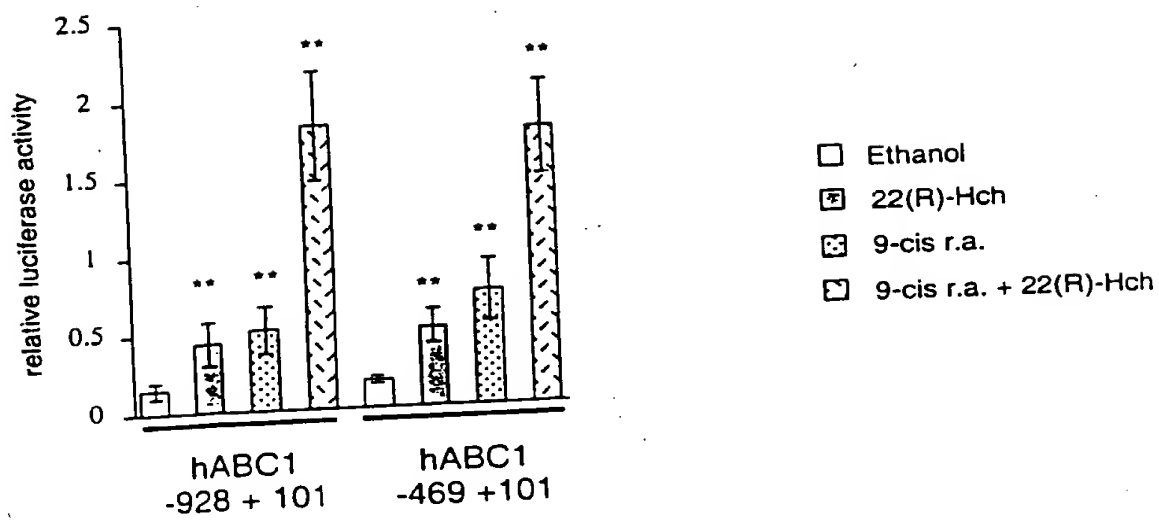
APPROVED	O.G. FIG.	
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FIG. 5A



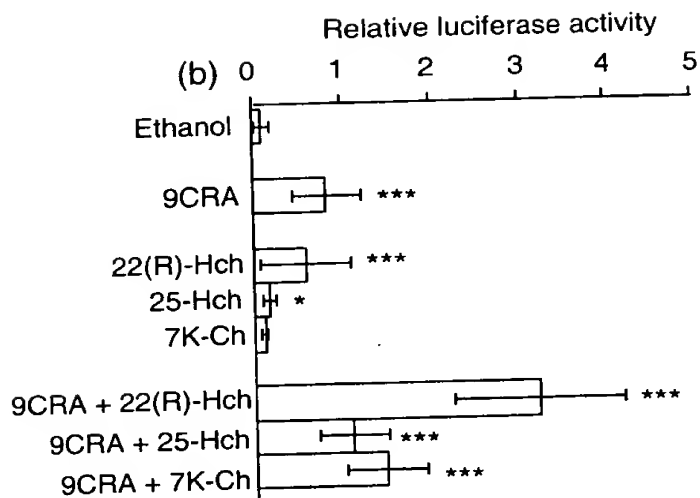
09560372-042800

FIG. 5B



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FIG. 5C



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FIG. 6A

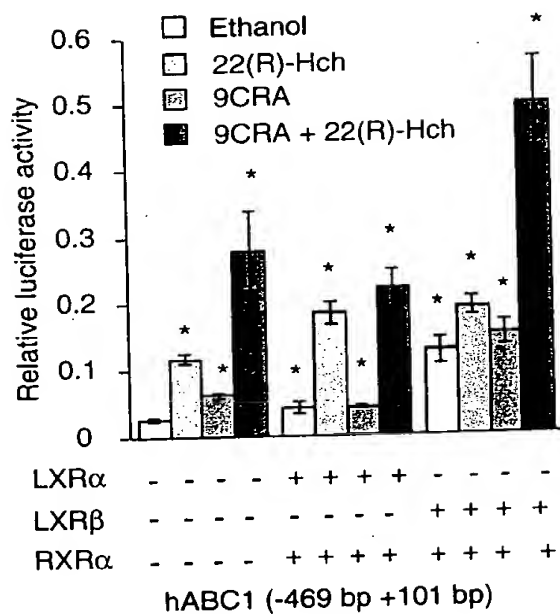
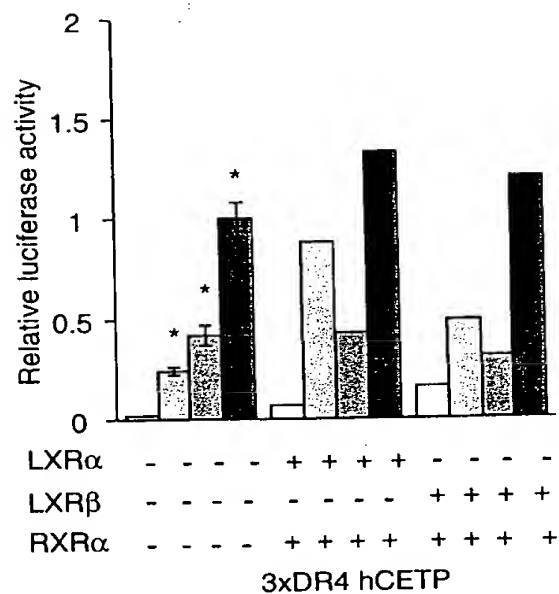


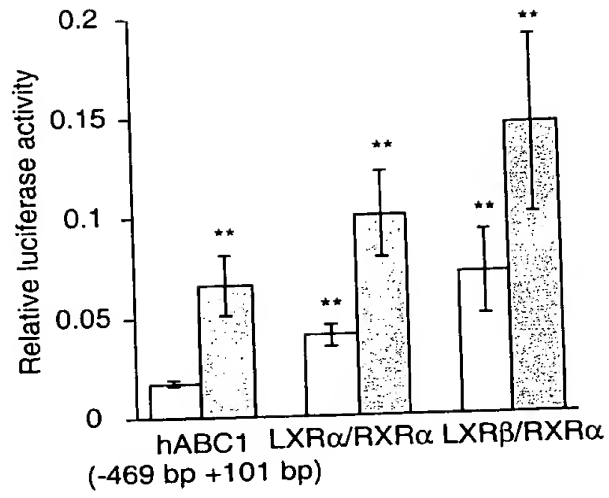
FIG. 6B





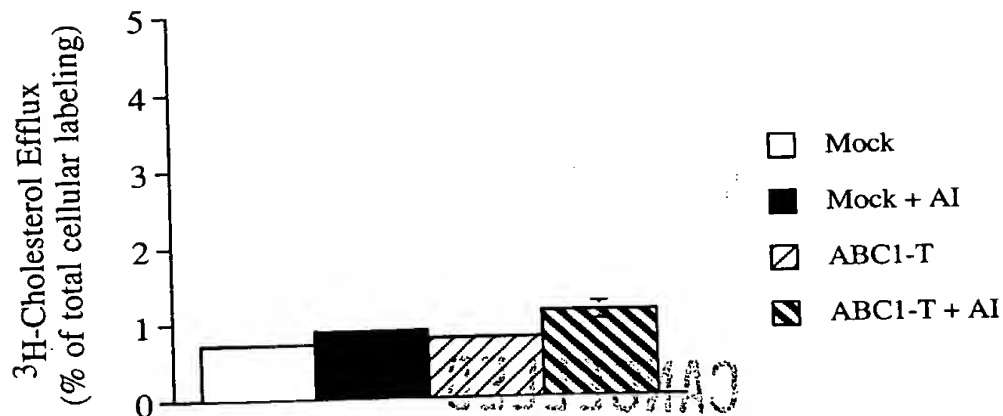
APPROVED	O.G. FIG.	
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FIG. 7



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FIG. 8A



ABC1-T: 61 MPSAGT--- (Genebank Accession: X75926; the methionine 61 here was originally designated as the start methionine. This version of cDNA is inactive in stimulating cholesterol efflux.)

FIG. 8B

